

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM nucleic - nucleic search, using sw model

Run on:

February 3, 2000, 14:17:29 ; Search time 49779.6 seconds  
(without alignments)  
-75.331 Million cell updates/sec

45: gb\_htg7: \*  
46: em\_htg1: \*  
47: em\_htg2: \*  
48: em\_htg3: \*  
49: em\_htg5: \*  
50: gb\_p13: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Title:

perfect score: US-08-962-560A-3

Sequence: 1235 CGAGCTCAAGCTCCGGCG . . . . . AGAAAAAAAAMAAAAA 1235

## Scoring table:

IDENTITY.NUC GapCp 10.0 , GapExt 1.0

## Searched:

821193 seqs, -1518192014 residues

## Total number of hits satisfying chosen parameters:

1642386

## Minimum DB seq length:

0

## Maximum DB seq length:

1000000

## Post-processing:

Minimum Match 0% Listing first 45 summaries

## Database :

GenEmbl:\*

1: gb\_bai:\*

2: gb\_ba2:\*

3: gb\_com:\*

4: gb\_cov:\*

5: gb\_pat:\*

6: gb\_ph:\*

7: gb\_p11:\*

8: gb\_p12:\*

9: gb\_prl:\*

10: gb\_p2:\*

11: gb\_pr3:\*

12: gb\_ro:\*

13: gb\_sts:\*

14: gb\_sy:\*

15: gb\_un:\*

16: gb\_v1:\*

17: em\_fun:\*

18: em\_hum1:\*

19: em\_hun2:\*

20: em\_lin:\*

21: em\_lom:\*

22: em\_or:\*

23: em\_lov:\*

24: em\_lpat:\*

25: em\_ph:\*

26: em\_lpl:\*

27: em\_lro:\*

28: em\_sts:\*

29: em\_sy:\*

30: em\_lun:\*

31: em\_v1:\*

32: gb\_htc1:\*

33: gb\_htc2:\*

34: gb\_in1:\*

35: gb\_in2:\*

36: em\_bal:\*

37: em\_ba2:\*

38: em\_hun3:\*

39: em\_hum4:\*

40: gb\_pr4:\*

41: gb\_htg3:\*

42: gb\_htg5:\*

43: gb\_htg6:\*

44:

## Result

## No.

## Score

## Query

## Match

## Length

## DB

## ID

## Description

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## SUMMARIES

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## -----

## ALIGNMENTS

RESULT 1  
MMRGNNS MMRGNNS 13812 bp DNA ROD  
LOCUS DEFINITION M.musculus PRM1, PRM2, PRM3 and TNP1 genes.  
ACCESSION Z47352.1 GI:136004  
VERSION 247352.1  
KEYWORDS PRM1 gene; PRM2 gene; PRM3 gene; protamine; TNP2 gene; transition

gb\_htg7: \*  
em\_htg1: \*  
em\_htg2: \*  
em\_htg3: \*  
em\_htg5: \*  
gb\_p13: \*

MURPIOD Human putative protein AC017106 Homo sapi  
AC015468 CNS01BNS ALI14464 Botrytis AC016253 Homo sapi  
ALI33219 Streptomyces AC013505 Homo sapi

AF132297 Homo sapi  
AC016253 Homo sapi  
AF27852 Human DNA sequence AC016188 Homo sapi  
Continuation (4 of 4) AC011100 Homo sapi  
ALI17194 Homo sapi  
AC015866 Homo sapi  
AC010404 Homo sapi  
AC017014\_1 Continuation (2 of 2) AC013648 Homo sapi  
AC011100 Homo sapi  
MURPIOD Human putative protein AC017106 Homo sapi  
AC015468 CNS01BNS ALI14464 Botrytis AC016253 Homo sapi  
ALI33219 Streptomyces AC013505 Homo sapi

SOURCE	Protein 2.	SEGEEEEDDEEEEEEQQIPVKGLLLEPERQESADEQAQPSPERKQTHS
ORGANISM	house mouse.	"
REFERENCE	Mus musculus	
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;	
JOURNAL	Rodentia; Sciurognathi; Muridae; Murinina; Mus.	
TITLE	Schlueter, G. and Engel,W.	
REMARK	Genomic sequence of the mouse protamine gene cluster	
REFCODE	Unpublished	
AUTHORS	2 (bases 1 to 13812)	
TITLE	Schlueter, G.	
JOURNAL	Direct Submission	
REMARK	Submitted (06 JAN 1995) Schlueter G. Institut fuer Humangenetik, Universitaet Goettingen, Gosslerstr.12d, Goettingen, germany, 37073	
REFCODE	Revised by [3]	
AUTHORS	3 (bases 1 to 13812)	
TITLE	Schlueter, G.	
JOURNAL	Direct Submission	
REMARK	Submitted (30 MAR 1996) Schlueter G. Institut fuer Humangenetik, Universitaet Goettingen, Gosslerstr.12d, Goettingen, germany, 37073	
REFCODE	4 (bases 1 to 13812)	
AUTHORS	Schlunger, G., Celik,A., Obata, R., Schlicker,M., Hoffeber, S., Schlunger, A., Adham, I.M. and Engel,W.	
TITLE	sequence analysis of the conserved protamine gene cluster shows that it contains a fourth expressed gene	
JOURNAL	Mol. Reprod. Dev. 43 (1), 1-6 (1996)	
MEDLINE	96341725	
COMMENT	On Jun 5, 1996 this sequence version replaced g1:88691.	
FEATURES	Related sequences: X07625, X07626, M60354.	
source	Location/Qualifiers	
gene	1. .13812 /organism="Mus musculus" /strain="cl29" /db_xref="taxon:10090" /chromosome="16"	
CDS	653. .902 /gene="Prml" /join(653. .758,853. .902) /note="male germcell specific, haploid expressed; chromatin binding" /codon_start=1 /product="protamine 1" /protein_id="CA87410_1" /db_xref="GI:136005" /db_xref="SWISS-PROT:P02319" /translation="MARYRCRSRSRCCCCRRRRCCRRRRCCRRRSYTRKRY" gene 5.817 /gene="Prml2" /join(5389. .5647,5753. .5817)	
CDS	/gene="Prml2" /note="Description: male germcell specific, haploid expressed; chromatin binding" /codon_start=1 /product="protamine 2" /protein_id="CA87411_1" /db_xref="GI:136006" /db_xref="SWISS-PROT:P07978" /translation="MVRKRSPPSPPGPGDWERERQGGAGGLSPERVEYGRHRRHH" gene 6.698. .6806 /gene="Prml3" /note="male germcell specific, haploid expressed" /codon_start=1 /product="protamine 3" /protein_id="CA87412_1" /db_xref="GI:136007" /db_xref="SWISS-PROT:Q61100" /translation="MGSRCSKLSTIGHEQPAQNTCHNRGHESSEKKLVACVSQDNFLS	
BASE COUNT	3400	ORIGIN
	a 3514 c 3869 g 3029 t	
ORIGIN		
Query Match	98 %	Score 1218; DB 12; Length 13812;
Best Local Similarity	99.6%	Pred. No. 2.6e-10; Matches 1221; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Matches	1221	
Match	CGAGGCTCAGCTCGGGGGATCTGCCGCGCTCAGCTGGGTCTGACC	60
Db	12356 CGAGGCTCAGCTCGGGGGATCTGCCGCGCTCAGCTGGGTCTGACC	12415
Qy	61 GGCTCTGCAACCGACGCCGCCTGACTGCCCTGCTCCATGAGCGAGCCCG	120
Db	12416 GGCTCTGCAACCGACGCCGCCTGACTGCCCTGCTCCATGAGCGAGCCCG	12475
Qy	121 GACGCTATGCCAACCCCTCAGCTGGCCCTCAGTAGTAGATGTAGCACCGT	180
Db	12476 GACGCTATGCCAACCCCTCAGCTGGCCCTCAGTAGTAGATGTAGCACCGT	12535
Qy	181 GGCACCCGACAAATGCCATCTCCGGCAGAGGCCCGACGCCGTCAGASCCCTCTC	240
Db	12536 GGCACCCGACAAATGCCATCTCCGGCAGAGGCCCGACGCCGTCAGASCCCTCTC	12595
Qy	241 GTCCTCGTCCTGCCAGGGCCCCGGCTCCGGCCCTCCGGCCCTGGCTCC	300
Db	12596 GTCCCTGTCCTGCCAGGGCCCCGGCTCCGGCCCTGGCTCC	12655
Qy	301 AGCCCAAGCCCTGGCAGACTCACTCACTCGCACCTCGCTCCACACTCGAATTACCGCG	360
Db	12655 AGCCCAAGCCCTGGCAGACTCACTCACTCGCTCCACACTCGAATTACCGCG	12715
Qy	361 CATACGGGACCAAGCGCCCTCCCTGGACGCCCTGGCTCTTGGAACCCCTGACCGT	420
Db	12716 CATACGGGACCAAGCGCCCTCCCTGGACGCCCTGGCTCTTGGAACCCCTGACCGT	12775
Qy	421 GCAGGGGCCACAGCGCCTGGCTGGAGGCCGCTGGCAACTTCTCTGGCTGGAG	480
Db	12776 GCACGGGGGCCACAGCGCCTGGCTGGAGGCCGCTGGCAACTTCTCTGGCTGGAG	12835
Qy	481 TGTGCAACGGACTCTCGGCTCAGCTGGAGATGCTCGGGCCCACAGAGAT	540
Db	12836 TGCACGGGACAGCTCTCCGGCTCAGCTGGAGATGCTCGGGCCCACAGAGAT	12895
Qy	541 CCGCTGCACTTCAGGGCGCCCTCACTGGACGCCACCGCGACCTCTGACTG	600
Db	12896 CCGCTGCACTTCAGGGCGCCCTCACTGGACGCCACCGCGACCTCTGACTG	12955
Qy	601 CCTTTGAGCTCTGGACACTACGGGAGCTGGAGATGCTCGGGCCCACAGAGAT	660
Db	12956 CCTTTGAGCTCTGGACACTACGGGAGCTGGAGATGCTCGGGCCCACAGAGAT	13015
Qy	661 GCGCAGCCGGCTGGCCGGCTCAGGGCTGGGCGCCAGCGCAGCGAGACCTCTGACTG	720
Db	13016 GCGCAGCCGGCTGGCCGGCTCAGGGCTGGGCGCCAGCGCAGCGAGACCTCTGACTG	13075
Qy	721 GGGCCGAGAACCTGGCGGCATCCCTCTAACCGGTACTCCGTACTACCTGACTC	780

Db	13076	GAGTCGCGAAGAACCTGGCGCATCCCTTAACCGGACTCTGGTACTCGTACTCAGATC	13135
Oy	781	CTTCCCCTTCAAGATCTGCCGCTGCCCTGCCGCTTAAAGGGGGCCCTA	840
Db	13136	CCTCCCTTCCAGATCTGCCGCTGCCGCTTAAAGGGGGCCCTA	13195
Oy	841	TTATTCCTATATAATTATATATATTTCTGGAACCAACCGTGGAGCCCTCCGCCT	900
Db	13196	TTATTCCTATATAATTATATATTTCTGGAACCAACCGTGGAGCCCTCCGCCT	13255
Oy	901	GGGTCSGAGGGGGTGTGAGATGCTCCACTCTGGTGGAGACTCAT	960
Db	13256	GGGTGGAGGGGGTGTGAGATGCTCCACTCTGGTGGAGACTCAT	13315
Oy	961	CCACCTCTAGGGGGCTCTCCCCCTCGGTCTCCCGGCTCCCGCTCTGT	1020
Db	13316	CCACCTCTAGGGGGCTCTCCCCCTCGGTCTCCCGGCTCCCGCTCTGT	13375
Oy	1021	GTAGCAGCTGTCCTGGCCAGGCTTCCACTCTACCTCTCATTTAGT	1080
Db	13376	GTAGCAGCTGTCCTGGCCAGGCTTCCACTCTACCTCTCATTTAGT	13435
Oy	1081	ATTCAGCTATCTGACCAACCAGGGTCGGGAGGGCTCTGGCTATTTGCG	1140
Db	13436	ATTCAGCTATCTGACCAACCAGGGTCGGGAGGGCTCTGGCTATTTGCG	13495
Oy	1141	TGTGCGAGTATCTTATTTACAGCCAGTTAGGATAACTTATATGGA	1200
Db	13496	TGTGCGAGTATCTTATTTACAGCCAGTTAGGATAACTTATATGGA	13555
Oy	1201	AAGTTTTTAAAGAAAGAAA	126
Db	13556	AAGTTTTTAAAGAAAGAAA	13581
RESULT	2		
MRN	MR088325		
LOCUS	MMU88325	1185 bp mRNA	ROD
DEFINITION	Mus musculus suppressor of cytokine signalling-1 (SOCS-1)	(SOCS-1)	06-JUL-1997
COMMENT	complete cds.	mRNA,	
ACCESSION	U88325		
VERSION	U88325.1	GI:2245381	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
REFERENCE	Euheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
AUTHORS	1 (bases 1 to 1185)		
JENKINS, R., WILLSON, T.A., VINEY, E.M., MURRAY, L.J.L., RAYNER, J.R., GONDA, T.J., ALEXANDER, W.S., METCALF, D., NICOLA, N.A.			
JENKINS, B.J., HILTON, D.J.			
ARTICLE	A family of cytokine-inducible inhibitors of signalling		
JOURNAL	Nature	387 (6636), 919-921 (1997)	
MEDLINE	97345633		
REFERENCE	2. (bases 1 to 1185)		
AUTHORS	STARR, R., WILLSON, T.A., VINEY, E.M., MURRAY, L.J.L., RAYNER, J.R., JENKINS, B.J., GONDA, T.J., ALEXANDER, W.S., METCALF, D., NICOLA, N.A.		
JOURNAL	Submitted (04-FEB-1997) Cancer Research Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, VIC 3050, Australia		
FEATURES	Location/Qualifiers		
source	1..1185		
	/organism="Mus musculus"		
	/chromosome="16"		
	/tissue-type="thymus"		
	/db_xref="Taxon:10090"		
gene	119..757		
CDS	/gene="SOCS-1"		
	119..757		
	/gene="SOCS-1"		
BASE COUNT	183 a 413 c 334 g 255 t		
ORIGIN	RMLCPLRORVRVQELCORTIAVGRENLAIRPLNPVLDYLSSFPQI*		
Query Match	90.6%	Score 1119.2;	DB 12;
Best Local Similarity	97.2%	Pred. No. 1.8e-192;	Length 1185;
Matches	1139,	Conservative 0;	Mismatches 33;
		Indels 0;	Gaps
Oy	56	TGGCGGCCCTGCGACCCGACGCGCGCTACCGCTCTGCTCCCTCATCGCG	115
Db	14	TGGCGACAGCCGCCCGAACCCGGCCGGCTCCCGTCCAGTGAGTAGATGAGTCACGACG	73
Oy	116	CCCCGACGCTATGCCACCCCTCAGCTGGCCCTCGAGTAGATGAGTCACGCCAC	175
Db	74	CCCCGACGCTATGCCACCCCTCAGTGAGTAGATGAGTCACGACG	133
Oy	176	CAGGTGGACGCCAGAATGGATCCTCCGGCAGGAGAGGCCGGGGCTAGAGCCC	235
Db	134	CAGGGCGACGCCAGAACATGGATCTCCGGCAGCGGCCCGAGGCCGAGGCC	193
Oy	236	TCCTGTCTCGCTCTGCTCTCGCAGCGGCCCGCTGGCTCCGGCTGCGG	295
Db	194	TCTGTCTCGCTCTGCTCTCGCAGCGGCCCGTGGCTCCGGCTGCGG	253
Oy	296	GTCCCCAGGCCAGCCCTGGCAGACTCTACTTCCACCTCCGATTAC	355
Db	314	CGGGCATCACGGGACACAGCGCTCCGGCTGCGCTGCGCTTATGGAGCCCT	373
Db	254	GTCCCAAGCCCGACGCCCTGCGACACTACACTCCACCTTCCGCTCCACTCCGATTC	313
Oy	356	CGGGCATCACGGGACACAGCGCTCCGGCTGCGCTGCGCTTATGGAGCCCT	415
Db	476	GACAGTCGTCACGCACTCTCTCGCTGAGATGCTGGCCACCTGGGACCCAG	535
Db	434	GACAGTCGCAACGGAACCTGCTCTCGCTCGCTCACGCTGAGATGCTGGGACCCAG	493
Oy	536	AGCATCCGGCTGCACTTCAGGCCGCCGCTTCACTGGACGGAGCCGGAGACCTTC	595
Db	494	AGCATCCGGCTGCACTTCAGGCCGCCGCTTCACTGGACGGAGCCGGAGACCTTC	553
Oy	596	GACGGCTTTCGAGCTGGCGGAGGACTAGTGGGGCGCGCGCGCGCAGTGTGGGGCC	655
Db	554	GACGGCTTTCGAGCTGGCGGAGGACTAGTGGGGCGCGCGCGCAGTGTGGGGCC	613
Oy	656	CGCGCGCCAGCGSCCGCGCGCGCGCTCAGGNGCTGCTGCGCATCCGGCC	715
Db	614	CGCGCGCCAGCGSCCGCGCGCGCTCAGGNGCTGCTGCGCATCCGGCC	673
Oy	716	GGCGGGGGCGGAGAACCTGGCGCATCCCTTAACCGGACTCTGGTACTCTGG	775
Db	674	GGCGGGGGCGGAGAACCTGGCGCATCCCTTAACCGGACTCTGGTACTCTGG	733
Oy	776	AGTTCCTTCGCTCAGATGCGGGCGCTGTGCGCACATTAGTGGGGGG	835
Db	734	AGTTCCTTCGCTCAGATGCGGGCGCTGTGCGCACATTAGTGGGGGG	793
Oy	836	CCTTATTCATTTCTGAAACCCAGTGGCGCTCC	895
Db	794	CCTTATTCATTTCTGAAACCCAGTGGCGCTCC	853
Oy	896	CGCGGGGGAGGAGTGTGCGGAGGATGCTCCACTCTGGTCTGAGAC	955



QY	1136	TCTGCTGTGAGATAATCCTAATTATTTACAGCCAGTTTASGTAATAACTTAT	1195	QY	296	GTCCCCASGCCAGCCCTGGCAACTCACCTCGCACCTTCGCTCCACCTCGGATTAC	355
Db	1105	TCTGCTGTGAGATAATCCTAATTATTTACAGCCAGTTTASGTAATAACTTAT	1164	Db	270	GTCGCCAGCCACGCCCCCTGGCAACTCACCTCGCACCTTCGCTCCACCTCGGATTAC	329
QY	1196	TATGAAAGTTTTTAAAGAAAAAA	1224	QY	356	CSCGCATCACGGGACAGGGCTCTGAGCCCTCGGCTTCTGGGACCCCTG	415
Db	1165	TATGAAAGTTTTTAAAGAAAAAA	1193	Db	330	CSCGCATCACGGGACAGGGCTCTGAGCCCTCGGCTTCTGGGACCCCTG	389
RESULT	4			QY	416	ASCGTGCAAGGGGCCAGAGGGCTCTGAGCCCTCGGCTTCTGGGACCCCTG	475
AF180302				Db	390	ASCGTGCAAGGGGCCAGAGGGCTCTGAGCCCTCGGCTTCTGGGACCCCTG	449
LOCUS	AF180302	1177 bp	mRNA	Db	510	AGCATCGCGTCACTCCASCCGGCGCTTCACTGGAGGGCACCGGGAGACCTC	595
DEFINITION	Mus musculus suppressor of cytokine signalling-1 (Socs1) mRNA,			QY	596	GACTGCCCTTGAGCTGCTGGAGCACTACAGGGCTTCACTGGAGGGCACCGGGAGACCTC	569
COMPLETE_CDS	complete cds.			Db	570	GACTGCCCTTGAGCTGCTGGAGCACTACAGGGCTTCACTGGAGGGCACCGGGAGACCTC	629
ACCESSION	AF180302			QY	656	CGCTGGCCACGGCAACTGCTGCTGGAGGGCTCTGGAGASCTGTGGCCAGCGCATCGTG	715
VERSION	AF180302.1			Db	630	CGCTGGCCACGGCCGCTGGAGGGCTCTGGAGAGGTGTGGCCAGCGCATCGTG	689
KEYWORDS				QY	716	GGCTGGCTGGAGACCTGGCGCATTCCTAACCGGTACTCCGACTACTG	775
SOURCE	house mouse.			Db	690	GGCTGGCTGGAGACCTGGCGCATTCCTAACCGGTACTCCGACTACTG	749
ORGANISM	Mus musculus			QY	776	AGTCCCTCCCTCCAGATCTGACCGCT3CCGCTGCCCCAGCTTAAGGGGGG	835
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				Db	750	AGTCCCTCCCTCCAGATCTGACCGCT3CCGCTGCCCCAGCTTAAGGGGGG	809
BUTHIERIA; Rodentia; Sciurognathi; Muridae; Murinae; MUS.				QY	836	CCCTTATTTCTCTTATTATTATTATTATTATTCTGGACCACCTGGAGCCCTTCC	895
REFERENCE	1 (bases 1 to 1177)			Db	810	CTTATTTCTCTTATTATTATTATTATTCTGGACCACCTGGAGCCCTTCC	869
AUTHORS	Gregoireff,A., Pyronnet,S., Sonenberg,N and Veillette,A.			QY	896	CGCTGGCTGGAGGGCTCTGGAGGTGTTGGAGATCTGGAGAC	955
TITLE	Regulation of suppressor of cytokine signalling-1 (SOCS-1) expression by translational repression			Db	870	CGCTGGCTGGAGGGCTCTGGAGGTGTTGGAGATCTGGAGAC	929
JOURNAL	Unpublished			QY	956	CCTATCCACCTCTAGGGGGGGCTCCCTCCCTGGCTCCTCCCTGGGCTCCTCC	1015
REFERENCE	2 (bases 1 to 1177)			Db	930	CCTATCCACCTCTAGGGGGGGCTCCCTCCCTGGCTCCTCCCTGGGCTCCTCC	989
AUTHORS	Gregoireff,A., Pyronnet,S., Sonenberg,N and Veillette,A.			QY	1016	TGTTGAGCTCTGGCTCTGGGGCCAGGAACCTGTAATCCCTCACTCTTCACTGTT	1075
TITLE	Direct Submission			Db	990	TGTTGAGCTCTGGCTCTGGGGCCAGGAACCTGTAATCCCTCACTCTTCACTGTT	1049
JOURNAL	Submitted (24-AUG-1999) McGill Cancer Centre, McGill University, 3655 Drummond Street, Montreal, Quebec H3G 1Y6, Canada			QY	1076	TGATATACTCCGATCTTACAACCAAGGGTGGGGGGCTCTGGCTTCACTT	1135
FEATURES	Location/Qualifiers			Db	1050	TACATATTCCTCAGTATTTTACACCAAGGGTGGGGGGCTCTGGCTTCACTT	1109
source				QY	1136	TCTGCTGTGAGATAATCCTAATTATTTACGCCAATTTAGGTAATAACTTAT	1195
BASE_COUNT	171 a	420 c	340 g	Db	1110	TCTGCTGTGAGATAATCCTAATTATTTACGCCAATTTAGGTAATAACTTAT	1169
ORIGIN	171 a	420 c	340 g	QY	1196	TATGAAAG 1203	
Query Match	88.9%		Score 1098.4; DB 12; Length 1177;	Db	1170	TATGAAAG 1177	
Best Local Similarity	97.3%		Pred. No. 9, 9e-189; Matches 1117; Conservative 0; Mismatches 31; Indels 0; Gaps 0;				
QY	56	TGGCGCAGCTGTGCCACCGGGACGCCGGCTACTGGCTCTCTCCCCATCGGCCAG	115				
Db	30	TGGCGCAGAGCCGCCGGAGCCCGAGCGGGCTCTGGCTCTGGCCAGGGCG	89				
QY	116	CCCCGGAGCTATGCCACCCCTCACTGTGCCCTGGAGTAGGATGAGTACCA	175				
Db	90	CCCCGGAGCTATGCCACCCCTCACTGTGCCCTGGAGTAGGATGAGTACCA	149				
QY	176	CAGGGCAGCGACATGCGATCTCCCGCAGAGGCCGGCTAGAGCC	235	RESULT	5		
Db	150	CAGGGCAGCGACATGCGATCTCCCGCAGAGGCCGGCTAGAGCC	209	BTPRMNP2	BTPRMNP2	13187 DP DNA	ROD
DEFINITION	R.novaligous PRM1, PRM2, PRM3 and TNP2 genes.			ACCESSION	246939	GI:1359527	11-DEC-1996
VERSION	246939.1			KEYWORDS		PRM1 gene; PRM2 gene; PRM3 gene; protamine; TNP2 gene; transition	
Db	210	TCTCGTCTCTCTGTCCTCGCCAGCGGCCCGTGCGRCCCGGCCCTGGCGGGG	269				





Best Local Similarity 99.7%; Pred. No. 9.4e-154; Matches 906; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Db	781	CTTCGGGCGAGACCTCCTCCACCTCAGGGGTGGGGTGCCCCCTCGTGTCTC	840						
OY	1001	CCTCGGGGCCCGCCCTGGTGTAGCAGCTGTTGGCCAGGACCTAATCCACTC	1060						
Db	841	CCTCGGGGCCCGCCCTGGTGTAGCAGCTGTTGGCCAGGACCTAATCCACTC	900						
Db	1061	CTACCTCTCATGTATCACATTCCAGATCTTGACAGCTGTTGGCCAGGACCTAATCCACTC	1120						
OY	901	CTACCTCTCATGTATCACATTCCAGATCTTGACAGCTGTTGGCCAGGACCTAATCCACTC	960						
Db	1121	CCTCGGCCTCATTTCTCTGAGAGATACTTATTAAATTTAGGGTTTA 1180							
OY	961	CTCGGCTCATTTCTCTGAGAGATACTTATTAAATTTAGGGTTTA 1020							
Db	1181	GGTATAAACCTTATTATGAAAGTTTTTTAAAA 1216							
Db	1021	GGTATAAACCTTATTATGAAAGTTTTTTAAAA 1036							
RESULT	7								
LOCUS	AB000710	909 bp mRNA for stat-induced stat inhibitor-1, complete cds.							
DEFINITION	Mus musculus mRNA for stat-induced stat inhibitor-1, complete cds.								
ACCESSION	AB000710								
VERSION	ab000710.1								
KEYWORDS	stat-induced stat inhibitor-1; SSI-1;								
SOURCE	Mus musculus cDNA to mRNA, clone-lib:thymus cDNA.								
ORGANISM	Mus musculus								
REFERENCE	Kishimoto, T., Muridae; Murinae; Mus; Rodentia; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rattus norvegicus; Scuroornathl; Muridae; Murinae; Mus; Rodentia; Scuroornathl; Muridae; Murinae; Mus.								
AUTHORS	1 (bases 1 to 909)								
TITLE	Submitted (25-JAN-1997) to the DDBJ/EMBL/GenBank databases.								
JOURNAL	Tadamasa Kishimoto, Osaka University, Medical School, Yamadaoka 2-2, Suita 565, Japan (E-mail: matsumoto@imed3.med.osaka-u.ac.jp, Tel:+81-6-879-3831, Fax:+81-6-879-3839)								
REFERENCE	Naka,T., Narasaki,M., Hirata,M., Tomoshige,M., Minamoto,S., Nishimoto,N., Kajita,T., Yoshiizaki,K., Akira,S. and Kishimoto,T.								
AUTHORS	Structure and function of a novel STATs-induced inhibitor of STATs function-1(SIS-1)								
TITLE	Unpublished (1997)								
JOURNAL	3 (sites)								
REFERENCE	Naka,T., Narasaki,M., Hirata,M., Matsumoto,T., Minamoto,S., Aono,A., Nishimoto,N., Kajita,T., Taga,T., Yoshiizaki,K., Akira,S. and Kishimoto,T.								
AUTHORS	Structure and function of a new STAT-induced STAT inhibitor								
JOURNAL	Nature 387 (6636), 924-929 (1997)								
MEDLINE	97345635								
FEATURES	Location/Qualifiers								
source	1.. .909								
	/organism="Mus musculus"								
	/db_xref="taxon:101090"								
	/clone_id="thymus cDNA"								
gene	55.. .693								
CDS	/gene="SSI-1"								
	55.. .693								
	/gene="SSI-1"								
	/codon_start=1								
	/product="stat-induced stat inhibitor-1"								
	/protein_id="BA21539_1"								
	/db_xref="GI:22747474"								
	/translation="MWANQNOA DNA ISPAEPRRSRSPSSSSSPAPVPRPCP								
	LVRDSRQNCFFLPSVKASGPSPISRVFOAQRGDNRETDCFLLEHVAAPR								
	RMGAPLQRVRVPLQECRQRIVAAVORENLRAPUNPVLYDYLSSPFQI"								
BASE COUNT	121 a	338 C	274 G	176 T					
RESULT	8								
AC002286	AC002286	12589 bp	DNA	1512 13	compar	PR1	23-NOV-1999		
LOCUS									
DEFINITION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
MEDLINE									
FEATURES	Location/Qualifiers								
source	1.. .909								
	/organism="Mus musculus"								
	/db_xref="taxon:101090"								
	/clone_id="thymus cDNA"								
gene	55.. .693								
CDS	/gene="SSI-1"								
	55.. .693								
	/gene="SSI-1"								
	/codon_start=1								
	/product="stat-induced stat inhibitor-1"								
	/protein_id="BA21539_1"								
	/db_xref="GI:22747474"								
	/translation="MWANQNOA DNA ISPAEPRRSRSPSSSSSPAPVPRPCP								
	LVRDSRQNCFFLPSVKASGPSPISRVFOAQRGDNRETDCFLLEHVAAPR								
	RMGAPLQRVRVPLQECRQRIVAAVORENLRAPUNPVLYDYLSSPFQI"								
BASE COUNT	121 a	338 C	274 G	176 T					
RESULT	9								
AC002286	AC002286	12589 bp	DNA	1512 13	compar	PR1	23-NOV-1999		
LOCUS									
DEFINITION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									
TITLE									
JOURNAL									
MEDLINE									
FEATURES	Location/Qualifiers								
source	1.. .909								
	/organism="Mus musculus"								
	/db_xref="taxon:101090"								
	/clone_id="thymus cDNA"								
gene	55.. .693								
CDS	/gene="SSI-1"								
	55.. .693								
	/gene="SSI-1"								
	/codon_start=1								
	/product="stat-induced stat inhibitor-1"								
	/protein_id="BA21539_1"								
	/db_xref="GI:22747474"								
	/translation="MWANQNOA DNA ISPAEPRRSRSPSSSSSPAPVPRPCP								
	LVRDSRQNCFFLPSVKASGPSPISRVFOAQRGDNRETDCFLLEHVAAPR								
	RMGAPLQRVRVPLQECRQRIVAAVORENLRAPUNPVLYDYLSSPFQI"								
BASE COUNT	121 a	338 C	274 G	176 T					

ACCESSION genomic sequence, complete sequence.  
 AC002286\_1 GI:2160310  
 VERSION HRG.  
 KEYWORDS human  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 1289)  
 Kramer,J.A., Adams,M.D., Singh,G.B., Doggett,N.A. and Krawetz,S.A.  
 Extended analysis of the region encompassing the PRML->PRM2->rNP2  
 domain: genomic organisation, evolution and gene identification  
 J. Exp. Zool. 282 (1-2), 245-253 (1998)  
 98390623  
 2 (bases 1 to 1289)  
 Loftus,B.J., Kim,J.J., Sneddon,V.P., Kalush,F., Brandon,R.,  
 Fuhrmann,J., Mason,T., Crosby,M.L., Barnsteed,M., Cronin,L.,  
 Eichler,E.E., Harris,P.C., Venter,J.C. and Adams,M.D.  
 Genome duplications and other features in 12 Mb of DNA sequence  
 from human chromosome 16p and 16q  
 Genomics 60 (3), 295-308 (1999)  
 99425270  
 3 (bases 1 to 1289)  
 Adams,M.D.  
 Direct submission  
 Submitted (04-JUN-1997) The Institute for Genomic Research, 9712  
 Medical Center Dr., Rockville, MD 20850, USA  
 4 (bases 1 to 1289)  
 Adams,M.D., Loftus,B.J., Zhou,L., La Bombard,M., Kim,U.J.,  
 Venter,J.C., Kramer,J.A. and Doggett,N.A.  
 Direct submission  
 Submitted (28-AUG-1997) The Institute for Genomic Research, 9712  
 Medical Center Dr., Rockville, MD 20850, USA  
 Address all correspondence to:  
 Mark Adams  
 The Institute for Genomic Research  
 9712 Medical Center Dr.,  
 Rockville, MD 20850,  
 USA e-mail address: mdadamstigr.org. The cosmid location is on  
 chromosome 16p13.13. The orientation of the sequence is from Sp6  
 end to T7 end. Genes were identified by a combination of five  
 methods including: XGRAIL (available by anonymous ftp from  
 arthur.eprn.ornl.gov), Genefinder (Phil Green, University of  
 Washington), Genscan (Chris Burge, <http://genomic.stanford.edu/~chris/GENSCANW.html>) searches of the  
 complete sequence against a peptide database, and the EST database  
 at TIGR (<http://www.tigr.org/tdb/at/at.html>). A gene with homology  
 to another protein is annotated as the isoform of that protein.  
 Genes without peptide homology having spliced EST hits are termed  
 'unknown protein'. Genes encoding tRNAs are predicted by  
 tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).  
 FEATURES  
 source  
 1. 12589  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /chromosome="16"  
 /map="16"  
 /clone="protamine16"  
 complement(381..440);  
 /rpt\_family="Gc\_rich";  
 repeat\_region  
 complement(751..896);  
 /rpt\_family="GC\_rich";  
 repeat\_region  
 complement(1318..3361);  
 /rpt\_family="AT\_rich";  
 repeat\_region  
 complement(1572..1700);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(2627..2730);  
 /rpt\_family="GAAAG";  
 repeat\_region  
 complement(2846..3888);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(3026..3134);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(3458..3501);  
 /rpt\_family="CAAT";  
 repeat\_region  
 complement(3810..3902);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(3936..4240);  
 /rpt\_family="Alu";  
 repeat\_region  
 complement(4318..4367);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(4394..4455);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(4569..4864);  
 /rpt\_family="Alu";  
 repeat\_region  
 complement(6617..6705);  
 /rpt\_family="CAAA";  
 repeat\_region  
 complement(7025..7226);  
 /rpt\_family="AlusX";  
 repeat\_region  
 complement(7296..7445);  
 /rpt\_family="Alu";  
 repeat\_region  
 complement(7445..7614);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(8005..8310);  
 /rpt\_family="AlusX";  
 repeat\_region  
 complement(8358..8358);  
 /rpt\_family="GAAA";  
 repeat\_region  
 complement(8659..8659);  
 /rpt\_family="AlusX";  
 repeat\_region  
 complement(9009..9338);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(9331..9331);  
 /rpt\_family="Alu";  
 repeat\_region  
 complement(9842..9998);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(10416..10552);  
 /rpt\_family="MIR";  
 repeat\_region  
 complement(10557..10599);  
 /rpt\_family="POLY\_A";  
 repeat\_region  
 complement(10989..10989);  
 /rpt\_family="AlusX";  
 repeat\_region  
 complement(11234..11542);  
 /rpt\_family="Alu";  
 repeat\_region  
 complement(12198..12309);  
 /rpt\_family="MIR";  
 misc\_feature  
 complement(12203..12589);  
 /note="has high homology to Human nuclear  
 ribonucleoprotein particle (hnRNP) C protein."  
 BASE COUNT  
 3067 a 3233 c 3221 g 3068 t  
 ORIGIN  
 Query Match 58.8%; Score 725.6; DB 40; Length 12589;  
 Best Local Similarity 80.7%; Pred No. 1.3e-121; Indels 36; Gaps 12;  
 Matches 1004; Conservative 0; Mismatches 204; Gaps 12;  
 Db 131 CCTCTAGGGCGGGCGCGCGGGAGGCCCGCCCTGGAGTGTGGCGGCACCT 190  
 Qy 6 CTGCAAGCTGGGGAGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCGCT 65  
 Db 191 GCGGCCACCGGAGGCCGGCTACTGCTCTGCTCTGGCGAGGCCGGAGC 250  
 Qy 66 GTGCCACCGGAGGCCGGCTACTGCTCTGCTCTGGCGAGGCCGGAGC 124  
 Db 125 CTATGCCACCCCTTGAGTCGCCCTGAGTAGATGTAGCAAGCACCAAGGG 184  
 Db 251 CTATGCCACCCCTGCCCTGAGTCGCCCTGAGTAGATGTAGCAACACCAAGGG 310  
 Qy 185 GCGCAACTGCGATCTCCGGAGAGGCCGCGGCCCTGAGGCCCTCTCGTC 244  
 Db 311 GCGGACAATGCGATCTCCACAGCAGAGGCCGCGGCCGAGAACCTTCC---TCC 367  
 Qy 245 TCGCTCTGGCTCCGGCCAGGGCCCCGGTGGCTCCCGGCCCTGGGGTCAGGCC 304





Qy	425	GGGGCGCACAGGCCCTGCGAGGCCACCTCTGGTGCAGACTGCT	484	Hirofumi Mano, Jichi Medical School, Department of Molecular Biology; 3311-1 Yakuishi, Minamikawachi-Machi, Kawachi-gun, Techigi 329-04, Japan (E-mail:hmano@jichi.ac.jp, Tel:0285-44-2111(ex.3482), Fax:0285-44-8675)
Db	6124	GGGGCGCACAGGCCCTGCGAGGCCACCTCTGGTGCAGACTGCT	6183	REFERENCE AUTHORS TITLE JOURNAL MEDLINE
Qy	485	CAAGGAACCTGCTCTCGGCCCTAGGTGAGAGTGCTCGGCCCTGGCCGAGCCGTCACCTCTGGTGCAGACTGCT	534	Ohya, K., Kajigaya, S., Yamashita, Y., Miyazato, A., Hatake, K., Mura, Y., Ikeda, U., Shimada, K., Ozawa, K. and Mano, H.
Db	6184	CAGGGAACTGCTTTGCGCTTAACCTGGATGCCAGGGCGAGCTGCGACAGCCATGCC	6243	SOCS-1/JAB/SSI-1 can bind to and suppress Tec protein-tyrosine kinase. <i>J. Biol. Chem.</i> , 272 (43), 27178-27182 (1997)
Qy	545	GTGCACTTCAGGCCGCCCTCAGTGGACACTAGTGGGGCGGCCATGCTGGGGGCCATGCC	604	
Db	6244	GTGCACTTCAGGCCGCCCTAACCCTGGAGCTGCTGGGGGCCATGCC	6303	
Qy	605	TTCAGACTCTGGAGCACTAGTGCGGCCGCGCCATGTTGGGGGCCATGCC	664	
Db	6304	TTCAGACTCTGGAGCACTAGTGCGGCCGCGCCATGCC	6363	
Qy	665	CAGGCCGCGCTGGCGGCCATGCC	724	FEATURES SOURCE gene
Db	6424	CGCGAGAACCTGGCGCATCCCCCTACCCCCCTCGCGACTACCTGAGCTTC	6483	/organism="Homo sapiens" /db_xref="taxon:9606" /gene="tip3"
Qy	785	CCCTCCAGATCTACCGCGCTGGCGCTGCGCGCATGCCAGCGCATGTTGGATGCC	844	/note="similar to AB000676:JAB, /product="Tip3" /protein_id="BA23521.1" /db_xref="GI:2627029"
Db	6484	CCCTCCAGATTCACGGGAGCGCCCGCGCGTGCACGCGCATTAACGGATGCC	6543	/translation="MHNHQVADNASTAEPRRRPEPSSSSPAAPRPRCPA VPAPGDNHRFRSHDRYRTRASALLDAGFTWGLPSHAGERLRAEPVGFL VDRSRNRCFELSVKUASGPISIRVFOAERFHLDGSRSERFDCLSELLEHVAAPR MIGALRORVRVLQELCRORIVATGVRENLRAPLNPLVRLYSSPPQI"
Qy	845	TTCATTATAATTATTATTCTGGACACGCGGCCCTGGCTCCACTCTGGCTGGAGA	903	
Db	6544	TAT-----TGTATACTTGCGAACATGTTGGTACCTCCCGCTGG	6594	
Qy	904	TGGAGGAGCTGGTG --GAAGTGAATGCCACTCTGGCTGGAGA-----C	955	
Db	6595	TGGAGGAGCTGGGTAGGGGGGGCTCCGGCGTGGAGAGCGAGCG	6594	
Qy	956	CTCTCCACCTCTCAGGGCTGGGTGCT-----CCCTCTGGTCTCC	1011	
Db	6655	CGCAGACCCCTCTCACCTCTGAGGGCTCTCCCTCTGGTCTCC	6714	
Qy	1012	CCC---CTGGTGTGAGCAT-----TGTGCTGGCCAGGCTGAAT-----CCCTCTGGTCTCC	1063	
Db	6715	CCCTGGTGTGAGCAT-----TGTGCTGGCCAGGCTGAAT-----CCCTCTGGTCTCC	6774	
Qy	1064	CCTCTCAGTTACATTCAGTATTCAGGATCTGCAACACAGGG -TGGGGGGCT	1122	
Db	6775	CCTCTCAGTTACATTCAGTATTCAGGATCTGCAACACAGGGCT	6834	
Qy	1123	CTGGCTCATTTCTGCTGTGAGAATCTCTTTATTTTACGCCAGTTAGG	1182	
Db	6835	CTGGCTTATTTCTGCTGTGAGAATCTCTTTAT-TTAAAGTCAGTTAGG	6893	
Qy	1183	TAATTAACCTTATGAAAGTTTTTTAAAGAAAAAA 1224		
Db	6894	TAATTAACCTTATGAAAGTTTTTTAAAGAAAAAA 6935		
RESULT	11			
LOCUS	AB000734	1216 bp mRNA	PRI	18-NOV-1997
DEFINITION		Homo sapiens mRNA for TIP3, complete cds.		
ACCESSION	AB000734			
VERSION	AB000734.1	GI:2627028		
KEYWORDS	TIP3; TIP3.			
SOURCE	Homo sapiens blood B-lymphocytes cDNA to mRNA.			
ORGANISM	Homo sapiens			
REFERENCE	1 (bases 1 to 1216)	Primates; Catarrini; Homidae; Homo.		
AUTHORS	Mano, H.	Submitted (27-JAN-1997) to the DDBJ/EMBL/GenBank databases.		
JOURNAL				

FEATURES	SOURCE	AUTHORS	STARR,R., WILLSON,T.A., VINEY,B.M., MURRAY,L.J.L., RAYNER,J.R., JENKINS,B.J., GONDA,T.J., ALEXANDER,W.S., METCALF,D., NICOLA,N.A., AND HILTON,D.J.
Db	483 ACTGCTCTGGCGCTCAGGGTAAGATGGCTGGACCGACGGATCCGGCCCAAGGAGATCCGGCGGTGACT 542	DEFINITION	ACTGCCTTTCGCCCTTAGCTGAAGTGGCTGGACCGACGGATCCGGCCCAAGGAGATCCGGCGGTGACT
Db	552 TCCASSCCG3CGCTTCACTTGTGACGCCASCGCGAGACCTCGACTGCCTTTGAGC 611	REFERENCE	TCCASSCCG3CGCTTCACTTGTGACGCCASCGCGAGACCTCGACTGCCTTTGAGC
Db	543 TTCAAGCCGGCGCGCTTCACCTGGATGGCGACGGAGCTTGAGCTTCAG 602	AUTHORS	TTCAAGCCGGCGCGCTTCACCTGGATGGCGACGGAGCTTGAGCTTCAG
Db	612 TGCTGGAGCTTACCGNGCCGGCCGGCCATGTGGGCCCCCTGGCCACGGCG 671	KEYWORDS	TGCTGGAGCTTACCGNGCCGGCCGGCCATGTGGGCCCCCTGGCCACGGCG
Db	603 TGCTGGAGCTTACCGNGCCGGCCGGCCGGCGCATGCTGGGGCCCGCTGGCCACGGCG 662	KEYWORD SOURCE	TGCTGGAGCTTACCGNGCCGGCCGGCCGGCGCATGCTGGGGCCCGCTGGCCACGGCG
Db	672 GCGTGGGGCGCGCTTCACCTGGTGTGRCGACGGCATGGCCGGGGCTGGCGAGA 731	ORGANISM	GCGTGGGGCGCGCTTCACCTGGTGTGRCGACGGCATGGCCGGGGCTGGCGAGA
Db	663 GCGTGGGGCGCGCTTCACCTGGTGTGRCGACGGCATGGCCGGGGCTGGCGAGA 722	Eukaryote; Primate; Catarrhini; Hominidae; Homo.	GCGTGGGGCGCGCTTCACCTGGTGTGRCGACGGCATGGCCGGGGCTGGCGAGA
Db	672 GCGTGGGGCGCGCTTCACCTGGTGTGRCGACGGCATGGCCGGGGCTGGCGAGA 731	1 (bases 1 to 1094)	GCGTGGGGCGCGCTTCACCTGGTGTGRCGACGGCATGGCCGGGGCTGGCGAGA
Db	732 ACCTGGCGCGCATCCCTGTTAACCGGTACCTCGCTGACTACCTGAGTTCCTTCCC 791	Stair,R., Willson,T.A., Viney,B.M., Murray,L.J.L., Rayner,J.R., Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A., and Hilton,D.J.	ACCTGGCGCGCATCCCTGTTAACCGGTACCTCGCTGACTACCTGAGTTCCTTCCC
Db	723 ACCTGGCTCGCATCCCTCACCCGCTCTCGCGACTACCTGAGTTCCTTCCC 782	A family of cytokine-inducible inhibitors of signalling	ACCTGGCTCGCATCCCTCACCCGCTCTCGCGACTACCTGAGTTCCTTCCC
Qy	792 AGATCTGACCGCTGCGCTGTGCGCAGCATTAAGTGGGGCGCTTATATTCTAT 851	TITLE	AGATCTGACCGCTGCGCTGTGCGCAGCATTAAGTGGGGCGCTTATATTCTAT
Db	783 AGATCTGACCGCTGCGCCCGCGTACCGCAGCATTAAGTGGATGGCTGCTTATT-- 840	JOURNAL	AGATCTGACCGCTGCGCCCGCGTACCGCAGCATTAAGTGGATGGCTGCTTATT--
Qy	852 TATAATATATATATTTCTGGAACCAACGTTGGGGCCCTCCC 910	Hall Institute of Medical Research, PO Royal Melbourne Hospital, VIC 3050, Australia	TATAATATATATATTTCTGGAACCAACGTTGGGGCCCTCCC
Db	840 -----TTGTTATTAATCTGCTGAACTATGGGTACCCCTCCGGCTGGTGGAGG 893	LOCATION/QUALIFIERS	-----TTGTTATTAATCTGCTGAACTATGGGTACCCCTCCGGCTGGTGGAGG
Qy	911 GAGTGGTTGAG---GAGGGTAGATGCTCCACTCTTGCTGGAGA- ---CCTCATC 962	1 . 1094	GAGTGGTTGAG---GAGGGTAGATGCTCCACTCTTGCTGGAGA- ---CCTCATC
Db	894 GAGCGGATGGGTGAGGGGGCGCCCTCGGGCGAGAC 953	/organism="Homo sapiens"	GAGCGGATGGGTGAGGGGGCGCCCTCGGGCGAGAC
Qy	963 CACCTCTCAAGGGTGGGGCTT---CCCTCCCTGCTGCTCCGGGCCCCC--CT 1016	/ab_xref="GR:25384"	CACCTCTCAAGGGTGGGGCTT---CCCTCCCTGCTGCTCCGGGCCCCC--CT
Db	954 CCCTCTCACCCTCTGGGGGCTCTCCCTCTGCTGCTCCCTCTGGCTCCCTCTGGT 1013	/ab_xref="taxon:9606"	CCCTCTCACCCTCTGGGGGCTCTCCCTCTGCTGCTCCCTCTGGCTCCCTCTGGT
Qy	1017 GGTTGTTAGCTT---TGTGCTGGGGCAGGACTGATT--CCACTCTAACCTCC 1070	/cell_type="B lymphocyte"	GGTTGTTAGCTT---TGTGCTGGGGCAGGACTGATT--CCACTCTAACCTCC
Db	1014 TGTGTTAGCTTACTGTTCTGGAGCAGCTGACTGCACCTCTTCTC 1073	/cell_line="Raji cell line"	TGTGTTAGCTTACTGTTCTGGAGCAGCTGACTGCACCTCTTCTC
Qy	1071 ATGTTTACATTTCCAGTACTTGCACAAACCRAGGG--TGGGGAGGRTCTGCTT 1129	LOCUS	ATGTTTACATTTCCAGTACTTGCACAAACCRAGGG--TGGGGAGGRTCTGCTT
Db	1074 ATGTTTACATTTACCGTACTTGCACAAACCCAGGGTGGGGAGGRTCTGCTT 1133	DEFINITION	ATGTTTACATTTACCGTACTTGCACAAACCCAGGGTGGGGAGGRTCTGCTT
Qy	1130 CATTTCCTGTCAGAATTCRATTATTTTACGGCAGTTAGTAA 1189	PRIMER	CATTTCCTGTCAGAATTCRATTATTTTACGGCAGTTAGTAA
Db	1134 TATTTTCTCTGTGAGAACCTTATTTAT-TTTTAAGTCAAGTTAGTAATAA 1192	SEQUENCE	TATTTTCTCTGTGAGAACCTTATTTAT-TTTTAAGTCAAGTTAGTAATAA
Qy	1190 CTTATTATGAAAGTTTTTT 1212	COMMENT	CTTATTATGAAAGTTTTTT
Db	1193 CTTTATATGAAAGTTTTTT 1215	DESCRIPTION	CTTATATGAAAGTTTTTT
RESULT	12		
HSU88326	Locus HSU88326	LOCUS	HSU88326
	Definition Human suppressor of cytokine signalling-1 (SOCS-1) mRNA, complete cds	DEFINITION	1094 bp mRNA
U88326	Accession U88326.1	ACCESSION	GI:2245383
VERSTON	Keywords	KEYWORDS	human, Homo sapiens
		ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
		REFERENCE	1 (bases 1 to 1094)
		AUTHORS	Stair,R., Willson,T.A., Viney,B.M., Murray,L.J.L., Rayner,J.R., Jenkins,B.J., Gonda,T.J., Alexander,W.S., Metcalf,D., Nicola,N.A., and Hilton,D.J.
		TITLE	A family of cytokine-inducible inhibitors of signalling
		JOURNAL	Nature 387 (1997), 917-921 (1997)
		REFERENCE	97345633 (bases 1 to 1094)

VPAAPGDTHTFRSHADRITRASALIDACGFWGPISVHGAERLRAEPVSTFL  
YRDSPRNCFETALSVMASGTSTRYFHQGRFHLDGSRSFDCFLELLHYAAPP  
MIGAPIORRVRPIQELCRPRIVAYGRENLARIPLNPUVDYLSSPFI\*

BASE COUNT	a	c	g	t
154	396	316	9	216
ORIGIN				
Query Match	55.3%	Score 682.4;	DB 9;	Length 1082;
Best Local Similarity	83.4%	Pred. No. 8	2e-14;	
Matches	904;	Conservative	0;	Mismatches 146;
Indels	34;	Gaps	10;	
Db	1	CAGCGACCCCGACGCTATGCCACCCACCGCTGGCTCTGTAGTAGTTAG	60	
Qy	108	CACGCACCCCGGACCTATGCCACCCCTTCACTGGCCCTGGAGTAGTGGATGTAG	167	
Db	168	CACGACCCGGTGGACCCGACAATGGGACTCCCGGAGCAGCCCCGACGGGT	227	
Qy	61	CACACACCGAGGGCACAGCCGACAATCAGTGTCCACAGCAGAGCCGACGGGC	120	
Db	121	CAGAACCTTC--TCCTCTCCCTCTGCCCGGCCCGGCCGCGCGCGCT	177	
Qy	288	GGCCGGAGCTCCAGGCCCAASCCCTGGCAGACTCTTGACACTTCTGGCTCCACT	347	
Db	178	GGCCGGGGTCCGGGCCCGGCCCGGAGACGGACTTCGACATTGGTTCGACG	237	
Qy	348	CGGATACGGGCATCACGGGACANGGGCTCTGGAGCTCGGCCTCTGG	407	
Db	238	CGGATACGGGCATCACGGGACANGGGCTCTGGAGCTCGGCCTCTGG	297	
Qy	408	GACCCCTGGCTGACGGGGCACAGGGGACTGGCTGGCGAGCCGCTGG	467	
Db	298	GGCCCTGAGGGGGGAGGGGGGAGGGGGGAGGGGGGAGGGGGGACCTTC	357	
Qy	468	TGGTGGCGGAGCTGGCAAGAACGACTTGCTTGTGGCTGGCTGGAGGGCG	527	
Db	358	TGGTGGCGGAGCACGCCGAGCGGAACTGCTTTCGCCCTTGGCTGAGATGGCTCG	417	
Qy	528	GGCCGAGGACATCCGGTGGACTTCAGGGGGGGCTTCACTTGACGCCAGCGG	587	
Db	418	GACCCAGGAGCACCCGGTGGACTTCAGGGGGGGCTTCACTTGACGCCAGCGG	477	
Qy	588	AGACCTGGTGGACTCCCTTTCGAGCTGCTGGGACACTTGCTGGCTGG	647	
Db	478	AGACCTGGTGGACTCCCTTTCGAGCTGCTGGGACACTTGCTGGCTGG	537	
Qy	648	TGGGGGGCCGGCAGGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	707	
Db	538	TGGGGGCCCGCTGGCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	597	
Qy	708	TGGTGGGGACCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	767	
Db	598	TGGTGGGGACCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	657	
Qy	768	ACTACCTGGAGTCTCCCTCCAGTCTGGGGCATCCCTTAACCCGGTACTCGTG	827	
Db	658	ACTACCTGGAGTCTCCCTCCAGTCTGGGGCATCCCTTAACCCGGTACTCGTG	717	
Qy	828	TGGGGGGCTTATATCTTATATAATATATATATATATATATATATATATAT	887	
Db	718	TAATCTGGGATGGCTGTTATATATATATATATATATATATATATATATAT	768	
Qy	888	GGCTCCCG-SCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	943	
Db	769	ACCTCCCGCTGGGGTGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	828	
Qy	944	CTGGCTGGAGA---CCTCATCCCACCTCAGGGGGGGGGT---CCCTCTCG	994	
Db	829	TGGCTGGAGAGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	888	
Qy	995	GGCTCCCGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1048	

RESULT 13

AB005043 LOCUS AB005043 1082 bp mRNA for STAT induced STAT inhibitor-1, complete cds.

DEFINITION Homo sapiens mRNA for STAT induced STAT inhibitor-1, complete cds.

ACCESSION AB005043

VERSION AB005043.1 GI:2443364

KEYWORDS STAT induced STAT inhibitor-1.

SOURCE Homo sapiens cDNA to mRNA.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1082)

AUTHORS Minamoto,S.

TITLE Direct Submission

JOURNAL Submitted (21-JUN-1997) to the DDBJ/EMBL/GenBank databases. Sei Iro Minamoto, Osaka University, Internal Medicine III, Yamadaoka 2-2, Saita, Osaka 556, Japan (E-mail:minamoto@med.osaka-u.ac.jp, Tel:06-879-3833, Fax:06-879-3833)

REFERENCE 2 (sites)

AUTHORS Yamamoto, S., Ikegami, K., Ueno, R., Narasaki, M., Naka, T.,' Yamamoto, H., Matsumoto, T., Saico, H., Hosoe, S., and Kishimoto, T.

TITLE Cloning and functional analysis of new members of STAT induced inhibitor (SSI) family : SSI-2 and SSI-3 (1997)

JOURNAL Biochem. Res. Comm. 237, 79-83 (1997)

FEATURES source

/organism="Homo sapiens"  
(ab\_xref="taxon:9606"  
/note="SSI-1"  
/codon\_start=1  
/evidence="experimental"  
/product="STAT induced STAT inhibitor-1"  
/protein\_id="BA22431\_1"  
/ab\_xref="GI:2443365"  
/translation="MVAHQNOVADNAVSTAEPRRPEPSSSSSPAPRPCCPA

CDS



